Claims:

1. An isolated polynucleotide, comprising a polynucleotide sequence which codes for the sahH gene of coryneform bacteria, selected from the group consisting of

   a) polynucleotide which is at least 70% identical to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,

   b) polynucleotide which codes for a polypeptide that comprises an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID No. 2,

   c) polynucleotide which is complementary to the polynucleotides of a) or b), and

   d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c)

2. The polynucleotide as claimed in claim 1, which is capable of replication in coryneform bacteria.

3. The polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.

4. The polynucleotide as claimed in claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

5. The DNA as claimed in claim 2 which is capable of replication, comprising

   (i) the nucleotide sequence shown in SEQ ID No. 1, or

   (ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii), and optionally

(iv) sense mutations of neutral function in (i).

6. A DNA as claimed in claim 5 which is capable of replication, wherein the hybridization is carried out under a stringency corresponding to at most 2x SSC.

7. A polynucleotide sequence as claimed in claim 1, which codes for a polypeptide which comprises the amino acid sequence shown in SEQ ID No. 2.

8. A coryneform bacterium in which the sahH gene is enhanced.

9. Escherichia coli strain DH5αmcr/pEC-XK99sahHalex deposited as DSM 14316 at the Deutsche Sammlung für Mikroorganismen und Zellkulturen (German Collection of Microorganisms and Cell Cultures), Braunschweig, Germany.

10. A process for the fermentative preparation of L-amino acids comprising:

a) fermentation of the coryneform bacteria which produce the desired L-amino acid and in which at least the sahH gene or nucleotide sequences which code for it are enhanced,

b) concentration of the L-amino acid in the medium or in the cells of the bacteria, and

c) isolation of the L-amino acid.

11. The process as claimed in claim 10, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

12. The process as claimed in claim 10, wherein bacteria in which the metabolic pathways which reduce the formation

of the desired L-amino acid are at least partly eliminated are employed.

13. The process as claimed in claim 10, wherein a strain transformed with a plasmid vector is employed, and the plasmid vector carries the nucleotide sequence which codes for the sahH gene.

14. The process as claimed in claim 10, wherein the expression of the polynucleotide(s) which code(s) for the sahH gene is enhanced.

15. The process as claimed in claim 10, wherein the catalytic properties of the enzyme encoded by sahH are increased.

16. The process as claimed in claim 10, wherein for the preparation of L-lysine or L-methionine the coryneform microorganisms have one or more enhanced genes selected from the group consisting of

16.1 the dapA gene which codes for dihydrodipicolinate synthase,

16.2 the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

16.3 the tpi gene which codes for triose phosphate isomerase,

16.4 the pgk gene which codes for 3-phosphoglycerate kinase,

16.5 the zwf gene which codes for glucose 6-phosphate dehydrogenase,

16.6 the pyc gene which codes for pyruvate carboxylase,

16.7 the mqo gene which codes for malate-quinone oxidoreductase,

16.8 the lysC gene which codes for a feed-back resistant aspartate kinase,

16.9 the lysE gene which codes for lysine export,

16.10 the hom gene which codes for homoserine dehydrogenase

16.11 the ilvA gene which codes for threonine dehydratase or the ilvA(Fbr) allele which codes for a feed back resistant threonine dehydratase,

16.12 the ilvBN gene which codes for acetohydroxy-acid synthase,

16.13 the ilvD gene which codes for dihydroxy-acid dehydratase,

16.14 the zwa1 gene which codes for the Zwa1 protein.

17. The process as claimed in claim 10, wherein for the preparation of L-lysine or L-methionine, coryneform microorganisms are employed which have one or more attenuated genes selected from the group consisting of

17.1 the pck gene which codes for phosphoenol pyruvate carboxykinase,

17.2 the pgi gene which codes for glucose 6-phosphate isomerase,

17.3 the poxB gene which codes for pyruvate oxidase

17.4 the zwa2 gene which codes for the Zwa2 protein.

18. The coryneform bacterium which contains a vector which carries a polynucleotide as claimed in claim 1.

19. The process as claimed in claim 10, wherein microorganisms of the species Corynebacterium glutamicum are employed.

20. The process as claimed in claim 19, wherein the strain DSM5715/pEC-XK99EsahHalex is employed.

21. A process for preparing an L-methionine-containing animal feedstuffs additive comprising:

a) culture and fermentation of an L-methionine-producing microorganism in a fermentation medium;

b) removal of water from the L-methionine-containing fermentation broth (concentration)

c) removal of an amount of 0 to 100 wt.% of the biomass formed during the fermentation; and

d) drying of the fermentation broth obtained according to b) and/or c) to obtain the animal feedstuffs additive in the desired powder or granule form.

22. The process as claimed in claim 21, wherein microorganisms are employed in which further genes of the biosynthesis pathway of L-methionine are additionally enhanced.

23. The process as claimed in claim 22, wherein microorganisms are employed in which the metabolic pathways which reduce the formation of L-methionine are at least partly eliminated are employed.

24. The process as claimed in claim 22, wherein the expression of the polynucleotide(s) which code(s) for the sahH gene is enhanced.

25. The process as claimed in one or more of claim 21, wherein microorganisms of the species Corynebacterium glutamicum are employed.

26. The process as claimed in claim 25, wherein the strain DSM5715/pEC-XK99EsahHalex is employed.

27. The process as claimed in claim 21, wherein one or more of the following steps are additionally also carried out:

e) addition of one or more organic substances, including L-methionine and/or D-methionine and/or

the racemic mixture D,L-methionine, to the products obtained according to b), c) and/or d);

f) addition of auxiliary substances selected from the group consisting of silicas, silicates, stearates, grits and bran to the substances obtained according to b) to e) for stabilization and to increase storability; or

g) conversion of the substances obtained according to b) to f) into a form stable in rumen, by coating with film-forming agents.

28. The process as claimed in claim 21 or 27, wherein at least a portion of the biomass is removed.

29. The process as claimed in claim 28, wherein essentially 100% of the biomass is removed.

30. The process as claimed in claim 21 or 27, wherein the water content is up to 5 wt.%.

31. The process as claimed in claim 30, wherein the water content is less than 2 wt.%.

32. The process as claimed in claim 27, wherein the film-forming agents are metal carbonates, silicas, silicates, alginates, stearates, starches, gums or cellulose ethers.

33. An animal feedstuffs additive prepared as claimed in claim 21.

34. The animal feedstuffs additive as claimed in claim 33, which comprises 1 wt.% to 80 wt.% L-methionine, D-methionine, D,L-methionine or a mixture thereof, based on the dry weight of the animal feedstuffs additive.

35. A process for obtaining RNA, cDNA or DNA in order to isolate nucleic acids or polynucleotides or genes which code for adenosyl homocysteinase or have a high similarity to the sequence of the sahH gene, which comprises employing the polynucleotide comprising the

polynucleotide sequences as claimed in claim 1 as hybridization probes.